us-09-856-070-19.rge

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GenCore version 5.1 3 Copyright (c) 1993 - 2003 Compugen Ltd
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OM protein - nucleic search, using frame\_plus\_p2n model

January 16, 2003, 16-55-57; Search time 1144 56 Seconds Run on:

(without alignments)
330.553 Million cell updates/sec

1 KEELMLRLQDYEE 13 US-09-856-070-19 Perfect score: Sednence:

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2054640 seqs, 14751402878 residues Searched

Total number of hirs satisfying chosen parameters:

Maximum DB seq length: 200000000 Minimum DB seq length: 0

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Mammalia; Eutheria; Cetartiodaetyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Hos.
1. (bases 1-to 2514)
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Ezrin and esteomectin, two proteins associated with cell shape and
growth, are enriched in the locus coeruleus
Mol. Cell. Neurosci 4, 64-73 (1993)
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Turunen.o., Wingvist, R., Pakkanen, R., Grzeschik, K.H., Wahlstrom, T.
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Draft entry and computer readable sequence for [1] kindly submitted by O.Turunen, 31-AUG-1989. Location/Qualifiers
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PHYKLDKYKSAQEVRKEDHUGFKFRKFYFEDNAEEJUDITQKLFEUQKEGILSD
FIYTFFEIAVLLASYAVLARESAYNKEVIKSSYLSSERLIPQHYMOHKITKOMEDK
IQVWHAEHRGMLKDNAMLEYLKIAQULEMYGINYFEIRNKKGTPLMALGYIALGINIYE
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                             /db_xre1-"taxon:9606"
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/note "cytovillin 2"
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1 LysGluGluLeuMetLeuArgLeuGlnAspTyrGluGlu 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (25-JAN-1990) Hunter T., The Salk Institute, Molecular
Biology and Virology Laboratory, 10016 North Forrey Pines Road, San
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FLOVKEGILSDEIYGPFTAVLLGSYAVQAKFGGYNKFVHKSGYLSSERLIPQRVMDQ
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GVDALGINI YEKIÐÖKLT PÆ Í GPPWSETFNI SPNÍNKKFY Í RÆTUR VYFYAPPIFLET.
NKR TLOLCMGNHELYMKRIK PIÐ FLEVQÓMKAÐARBEKHÓKQI EKIÐOLFEKKRRRETVE
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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VINA cloning and Sequencing of the protein-tyrusine kinase substrate, eztin, reveals homology to band 4.1 
EMBO J. 8 (13), 4133-4142 (1989)
                                                                                                                                                                                                                                                                                                                      ezrin; kinase substrate; microvilli protein.
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/db_xref="G1:31283"
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                                                            US-09-856-070-19 (1-13) x AX411074 (1-3044)
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X51521 1 G1:31282
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3672 bp mRNA linear PRI 23 MAR-2000
Home siptons mPNA; cDNA DKF2p752H157 (from clone DKF2p762H157);
complete cds.
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information about the clone and the sequencing project is available
at http://www.mnps.biochem.mpg.de/projectNA/.
Loadup/Qualifiers
1. 3072
                                                PAT 28 JUN 2002
                                                                                                                                                                                 Homo sapiens
Eukaryddu, McLadda; Chordata; Graniara; Vertebrata; Euteleostomi;
Mammalia, Eutheria, Primates, Catarrhini; Hominidae; Homo.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                             Compositions and methods for the therapy and diagnosis of ovarian
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Ottenwaelder, B., Obermaler, B., Mewes, H.W., Weil, B. and Wiemann, S.
                                                                                                                                                                                                                                                                           Xu,J., Mitcham,J.L., Harlocker,S.L., Dillon,D.C., Secrist,H.,
Lodes,M.J., Alqate,P.A., Fling,S.P., Mannion,J., Benson,D.R. and
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                                                            Sequence 329 from Patent W00190154.
AX440476
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/db_xrref="taxon:9606"
687 c 856 g 675
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Source

indels:

100.008

Query Match:

US-09-856-070-19 (1-13) x HSEZPIN (1-3044)

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LKLDKKVSAQEVRKENPLQFKFRAKFYPEDVAEELLQDITQKLFFLQVKEGILSDEIY
CPPETAVLLGSYAVQAKHGDYNKEVHKSGYISSFPI IPQPVMFGHKLTPROQMEDPIQV
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                  /clone-*nkF*p762H157"
/tissue_type="melanoma (MeWo cell line)"
/clone_lib="762 (synonym: hmel2). Vector pSportl; host
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gone Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 41 Center Drive, Poor 11AC4, Betherda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens, Similar to villin 2 (ezrin), clone Moc.1584.
IMAGE:2959399, mRNA, complete eds.
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        Oy
        LysGluGluCuMetLenArgleuGlnAspTyrGluGlu 13

        Db
        1163 AAGGAGGTTGATGTGTGCTGCGGCTGCAGGACTATGAGGAG 1201

                                                                                                                                                                                                                                                                                                                                         /product-"hypothetical protein"
/protein_id="CAB82418.1"
/db_xref="G1:7328175"
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/organism-"Homo sapiens"
/db_xref-"taxon:9606"
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                                                                                                                                                                                                                                                                        /gene-"DKF2p7628157"
                                                                                                                                                                                                                       /qene="EKFXp762H357"
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Email: egapbs-ramail.nih.gov
                                                                                                                                               DHIOB; sites NotI + /dev stage "adult"
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Clone distribution: MGC clone distribution information can be found through the I M A G E Consertian/Lin. at: http://image.lln.gov
Series: IRAL Plate: 2 Row: a Column: 18
This clone was seisered for full length sequenting because it
passed the following selection criteria: matched mRNA qi: 9257254,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FGLHYVDNKGEPTWILKI.DKKYSAQEVYRENPI.QFKFRAKFYPEDVAEELJODITGKI.P
FLQVKEGII.SDETYCPPETAVI.LGSYAVQAKFGDYNKEVHKSGYI.SSERLJPQKVMDQ
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REKEQMMREKEELMLRLQDYEEKTKKAERELSEQIQRALQLEEEHKRAQEEAFRLEAD
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RDDRNEEKRTTEAEKNERVQKQLTTLSSELSQARDENKRTHNDTTHNEMAGGREKYK
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Human DNA sequence from clone RP11 507010 on chromosome 6425.2-26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (15-SEP-2001) Sanger Centre, Hinxton, Cambridgeshire, Call 18A, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests.clonerequest@sanger.ac.uk
on Sep 12, 2001 this sequence version replaced di:14586.248.
During sequence assembly data is compared from overlapping clones.
DNA Sequencina by: Institute for Systems Biology http://www.systemsbiology.org contact: amadan/systemsbiology.org contact: amadan/systemsbiology.org Anup Madau, Rachel Dickhoff, Jossica Fahey, Stephanie Ford, Julia Greene, Mark Retteman and Anuradha Madan
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product-"Similar to villin 2 (ezrin)"
                                                                                                                                                                                                                                                                                                                                                                                                              /tissue_type="Colon, adenocarcinoma"
/clone_lib-"NIH_MGC_15"
/lab_host="DH10B-R"
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/db_xref-"taxon:9606"
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Sehra, H.
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together with a note of the overlapping close name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping cloue, as we submit sequences with only a small everlar as the ribed the variation of this sequence was finished as follows unless otherwise noted. All regions were either double stranded or sequenced with an alternatic chemistry or covered by high quality data (i.e., phred quality > 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one MIS subclone; and the assertion of the continuous confirmed the context where the covered by at least and an attempt who continued the covered by at least than one plasmid subclone or more than one MIS subclone; and the
                                                                                                                                                                                                                                                                                                                   assembly was confirmed by restriction digest, the following abbrevial fours are used to associate primary accession nonlines given in the feature table with their source databases Fm. EMML Sw. SWISSPROID IT, IRRUMIL WP., WORMPER: Information on the WORMPER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 http://www.sanger.ac.uk/Projects/Cjelegans/wormpep This sequence
was generated from part of bacterial clone contrus of human
chromosome 6, constructed by the Sanger Centre Chromosome 6 Mapping
Group. Further information can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     lingar PRI 19-001-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RPI1-507010 is from the library RPCI-11.2 constructed by the group of Pieter de Jong. For further details see http://www-chori.org/larga/Jonm-htm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note-"Sequence from uni-directional primer reads only."
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This sequence is the entire insert of clone RFII-507C10 The true right end of clone RPII-114MIL is at 47323 in this sequence.

Location/Qualitiers
1. .215705
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Where differences are found these are annotated as variations
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        PHTHHHHHHHHHHHHHHHHHHHHH

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Padiel,A., Chen,Z.C. and Naftolin,F.
Mutation of ezrin gene in cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches:
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Best Local Similarity.
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A scue family consisting of ezrin, radixin and mossin. Its specific Jocalization at actin filament/plasma membrane association sites 9.0050012. Sci. 103 (Pt.1), 131-143 (1992)
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1EVQQMKAQAPEEKXQNQLEFQQLETEKKRPEXVEREKEQMMPEKEELMLKLQDYED
1 93 C 136 g 93 t 2 others
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Unpublished
2 (buses i to 478)
Endiel.A. Chen, Z.C. and Nattolln, F.
Lifediel.A. Shen, Shen, Shen, S.C. and Nattolln, F.
Lifediel.A. Shen, Shen, Shen, Shen, Shen, Shen, Shen, Shen, C. Sego, USA
New Haven, CT 66520, USA
New Haven, CT 66520, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fükatyota, Metazoa, Ohurdutu, Oruniatu, Vertebrata, Euteieostomi:
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae: Mus.
1. (bases 1-to-2701)
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Sato,N., Funayama,N., Naqafuchi,A., Yonemura,S., Tsukita,S. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (12-JUL-1991) N. Funayama, National Inst. for Physiological Sciences, Myodairi Okaraki 444, JAPAN 2 (bases 1 to 2701)
Punayama, N. Nagafurbi, A. Saro, N. Tsukita, S. and Tsukita, S. Radixin is a novel member of the band 4.1 lamily J. Cell Hiol. 115 (4), 1039-1048 (1991)
                                                                                                                                                                                                                                                                                                            /sote "villin 2; kisase substrate"
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/cell_line="HL60"
/cell_type="leukemia cells"
/l...>478
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                                                                                                                                                                                                                                                                                                                                                                      /protein_id="AAF03156.1"
/db_xref="G1:6063147"
                                                                                                                                                             /organism="Homo sapiens"
/db_xref-"taxon:9606"
/chromosome-"6"
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                                              AUTHORS
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/organism="Mus musculus"

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KEKKOMI PEK FELMI PLQEVYEQKTKPAEKELSEQTEKALQLEEEPRRAQEEAERLEAD
KMAAIRANELLEKQAQIQI NSQEQUAABLARY LAN LALLEKEKKREDIEVEBWQHKAN
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/translation-"MPKPINVRVTTMDAELEFAIQPNTTGRQLFDQVVKTIGLREVWY
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Mus musculus chromosome 16 elege RP23-3512, Webering (PAF) SEGGINGE,
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Submitted (15-JAN-2401) Production Sequencing Pacifity, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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Consensus quality: 129780 bases at least 040
Consensus quality: 150786 bases at least 030
Consensus quality: 159784 bases at least 020
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Unpublished
                                                                                                                                       /db xret-"MGD:MGI:98931"
                                  lib-"lambda qtll"
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Zdb xret="taxon:10090"
Zcell line="F9"
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Estimated insort size. 180802; sum-of-contins estimation forallty coverage. 3.02 in 020 bases: agarose to estimation Quality coverage. 3.34 in 020 bases; sum-of-contins estimation.

* NOTE: This is a "working draft' sequence. It currently consists of 26 contins. The true order of the pieces.

* is not known and their order in this sequence record is
                                                                                                                               * arbitrary, Gaps between the contigs are represented as * runs of N, but the exact since of the daps are unknown. This record will be applated with the limished sequence * as soon as it is available and the accession number will * be preserved.
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contig of 41175 bp in length.
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contig of 1022 bp in length
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gap of unknown length
contig of 1455 bp in length
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contig of 1163 bp in length
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (28.JUL-2000) Department of Molecular Genetics, Albert Binstein College of Medicine Genome Center, 1300 Morris Park Ave., Bronx, NY 10461, nSA 3 (bases 1 to 207782) Han, J. Montgomery, K.T., Padigaru, M., Grills.G., Loo.E., Loon J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (14-DEC-2001) Harvard Partners Center for Cenetics and Genemics, Harvard Medical School, 65 Landsdowne St., Cambridge, MA
                                                                                                                                                                                                                                                                                                                        Han, J., Montgomery, K.T., Grills, G., Lee, E., Long, J., Pomerantz, R., Ioshikhes, I.P., Shim, C., Decker, T., Thomas, E., Perera, A., Gordon, M., Goltz, J. S. and Kucherlapati, R. High Throughput Mouse Sequencing
                                                                                                                                                                                                                                                                                                     Rodentia; Sciurognathi, Muridae; Murinae, Mus.
                                                                                                                                                                                                                                                                                      Eukaryota, Mctazoa, Chordata, Craniata, Vertebrata, Eateleostomi)
Mammalia, Eatheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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Hab.J., Montgomery, K.T., Grills, G., Lee, E., Long, J., Pomerantz, P.
Ioshikhes, L.P., Skin, C., Leeker, J., Thomas, E., Ferera, A.,
Gordon, M., Gollz, J. S., and Kucherlapati, P.
Direct Submission
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Chemistry: Dye-terminator Big Dye; 1008
*Consensus quality: 185594 at least Q20
*Consensus quality: 177266 at least Q40
*Consensus quality: 174266 at least Q40
Estimated insert size: 4948 at least Q40
**Kimmated insert size: 206802 - sum-of-contigs
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Quality coverage: 4.8x sum-of-contigs - N/A
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Code: HPGC
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                       Conservative.
Mismatches:
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 Longth.
Matches.
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Ioshikhes, I.P. and Kucherlapati, R.
                                                                                   US-09-856-070-19 (1-13) x ACU875U5 (1-1833U2)
                                                              Gaps:
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Submitted (01-FEB-2000) Department of Molecular Genetics, Albert
Einstein Coilege of Medicine Genome Center, 1900 Marris Park Ave.,
                                                                                                                                                                                                                                                                                                                         Estimated insert $12e, agarose-Fr - NyA
**Estimated insert size; 27717 - sum-of-contias
Quality coverage: agarose-FP - NyA
Quality coverage: 6 5 x in u20 bases; sum-of-contigs estimation
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                                                               On Jan 4, 2002 this sequence version replaced gi:11094413.
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                                                                                                                                        Web site: http://www.hprqq orq/Sequence/mouse.html
Contact: hpgc@mendel.mgh.harvard.cdu
------Summary Statistics
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contig of 45600 bp in length
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215751. gap of unknown length
215800: config of 49 bp in length
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216675: contig of 855 bp in length
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                                                                                                                                                                                                                        Sequencing vector: pUC18; L08752
Chemistry: Dye-terminator Big Dye; 100%
*Consensus quality: 212564 at least 020
*Consensus quality: 211720 at least 030
*Consensus quality: 210397 at least 040
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             176158, .b04272
/mote="assembly_name:Contig207"
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142343. 176177
/note-"assembly_name:Contig208
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/note="assembly_name-Contig206"
                                                                                                Center: Harvard Partners Genome Center
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/note="assembly_name:Contig210
                                                                                                                                                                                                                      PUC18; L08752
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/rlone-"RP23-103120"
                                                                                 Genome Center
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106541. .142322
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Mammalia; Eutheria; Rodentia; Sciuroquathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Montgomery, K.T., Grills, G., Han, J., Low, F., Long, J., Pomerantz, P., Grahikhes, L.P., Shim, C., Decker, J., Thomas, E., Perera, A., Golle, J.S. and Kucherlapati, R. Bigh, Throughput, Mouse Sequencing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 (Dasos Lo 217917)
Montgomery, K.T., Grills, G., Han I., Los, B., Losy, L., Namerartz, P.,
Loshikhes, L.P., Shim, C., Dockor, J., Thomas, E., Perera, A.,
Gordon, M., Golls, J. S. and Kucherlapali, P.
Direct Submission
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205727: gap of unknown length
207782: contig of 2055 bp in length.
                                     contig of 1443 bp in length gap of anknown length
                                                                                                                     contig of 1383 bp in length
gap of unknown length
                                                                                                                                                                                                                                     contig of 1668 bp in length
gap of unknown length
190625: contig of 2715 bp in length
                                                                             contig of 1529 bp in length
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contig of 1228 bp in length
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gap of unknown length
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                     190645: qap of unknown length
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/chromosome-"15"
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* as seen as it is available and the accession number Will
     * is not known and their order in this sequence record is
                      * arbitrary, Gaps between the contigs are represented as * runs of N, but the exact sizes of the gaps are unknown.
• this record will be updated With the finished sequence.
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Mus musculus chromosome TNK clone PP24-342H13, WePKING DPART
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Enkaryota, Metazoa, Chorlata, Craniata, Vertebrata, Euteleostomi,
Mammalia: Eutheria, Abdentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (08-AUG-2002) Genema Sequencing Center, 4444 Forest Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   * NOIE: This is a 'working drait' sequence. It currently a consists of 10 run igs. The true order of the pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Center. Washington University Genome Sequencing Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Consensus quality: 233524 bases at least 040 consensus quality: 236724 bases at least 020 consensus quality: 236726 bases at least 020 lineart size: 225622, adative the size: 225622 adative the size: 304647 sum of reontias guality coverage: 14.29 in Q20 bases; agarose-fp ouality coverage: 8.54 in Q20 bases; sum-of-centigs
                                                                                                                                                                              227 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequencing vector: M13: 0%
Sequencing vector: plasmid; 100%
Chemistry: Dya-primer ET: 0% of reads
Chemistry: Dya-terminator Big Dye; 100% of reads
Assembly program: Phrap: varsion 0 940319
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209273. .214332

/note="assembly_name:Cont.q205"

214353. .215731

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215752. .215806

/note="assembly_name:Cont.g207"

215821. .215675

/note="assembly_name:Cont.g202"

216696 217917
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MCPherson, J.D. and Waterston, K.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nearest submission Materstein, F.H. Direct Submission Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Center project name: M_BE0342Hi3
                                                                                                                                                                                                                                                                                                                                          Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE, 10 unordered pieces. AC125143
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HTG; HTGS_PHASE1; HTGS_DRAFT.
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100.00%
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95.31%
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linear pai la-oci-lege
                 gap of unknown length
contig of 2982 bp in length
gap of unknown length
contig of 18201 bp in length
gap of unknown length
contig of 21961 bp in length
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                                                                                                                                                                                                                                                                                        contig of 123560 bp in length
                                                                                                                                                                                  gap of unknown leigth
contig of 26715 bp in length
app of unknown length
contig of 56889 bp in length
gap of unknown length
                                                                                                                                                               contig of 31906 bp in length
                                                                                                                                                                                                                                                                                                                              contig of 851 bp in length
gap of unknown length
contig of 1040 bp in length.
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1503: contig of 1503 bp in length
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AF188897
                                                                                                                                            gap of unknown length
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/note-"assembly_name:Contig101"
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/hote "assembly_hame:Contig102"
45048, .76953
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/note="assembly_name:Contigl03"
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/note-"assembly_name:Contigl04"
103869, 160757
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/note-"assembly_name:Contig100"
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ture 285469, 285508
/nute assembly_name:Contig79"
7835; a 64449 c 65769 g 77032 t
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/note="assembly_name:Contig99"
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/db_xrel-"taxon:9606"
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/map-"6q22-q27"
/cell_line="Bix3"
/cell_type-"epithelial cancer cells"
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/product-"ezrin"
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Search completed: January 16, 2003, 19:03:44 Job time : 1208.56 sees

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